

09/490,609



PATENT

IN RE APPLICATION OF

Bunch et al.

SERIAL NUMBER: 09/490,609

FILED: January 25, 2000

TITLE: BIOMARKERS AND ASSAYS FOR CARCINOGENESIS

SO-3170-US

GROUP ART UNIT: 1635

EXAMINER: David Fitzgerald

DATE: March 05, 2001

RECEIVED

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TECH CENTER 1600-2900

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**Commissioner of Patents and Trademarks, Washington D.C. 20231
on March 05, 2001.**

Rachel Polster

Rachel Polster Date 03/05/01

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STATEMENT UNDER 37 CFR 1.821 § (e)&(f)

Commissioner of Patents and Trademarks
Washington, D. C. 20231

Sir:

Please transfer to the above mentioned application, in accordance with 37 C.F.R. § 1.821(e), the computer readable copy(ies) from the applicant's parent application Serial No. 09/490,609.

This will confirm that the content of the paper copy and the computer readable copy of the Sequence Listing is the same as the sequence Listing to which it is indicated to relate.

Respectfully submitted,

Rachel A. Polster

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Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/492,609

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☒ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(1) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.
AKS-Biotechnology Systems Branch- 5/15/99

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/490,609DATE: 02/15/2000
TIME: 14:15:54

Input Set: I490609.RAW

This Raw Listing contains the General
Information Section and those Sequences
containing ERRORS.

E--> 1 <110> *insert mandatory response*
2 <120> CARCINOGENESIS_BIOMARKERS
W--> OK 3 <130>
4 <140> US/09/490,609
5 <141> 2000-01-25
6 <160> 580

*IMPORTANT: see item 5
in Error Summary sheet*

*Does Not Comply
Corrected Diskette Needed*

ERRORED SEQUENCES FOLLOW

*Due to size of listing, only first two
pages shown as a sample of global error*

7 <210> 1
E--> 8 <211> 271
9 <212> DNA
10 <213> Rattus norvegicus
11 <400> 1
E--> 12 gatccaccta acaagaagcc caaagtctag acgtgcctt ttgcctgtga
W--> 13
E--> 14 tgatttggtg 60
E--> 15 ctgcagggtg gccagcgtct gtctgatact aagtggtaaa tgaactacgt
W--> 16
17 gtttttatgg 120
E--> 18 gaaacaaaaa tatttttggta atcatcaaat ttatactagc tatctgggtg
W--> 19
20 ttagcatatc 180
E--> 21 tagtaattat gagtctagaa taatttttac atatttttat attattgtcc
W--> 22
23 tctcagttac 240
E--> 24 tgaatggatg gaaaacaatc atgttggttt a
25 271

*global format error - see item 1
in Error Summary sheet*

26 <210> 2
E--> 27 <211> 206
28 <212> DNA
29 <213> Rattus norvegicus
30 <400> 2
E--> 31 gatccaagac cctcgctgac tccgtctgaa tttttgggtt cagtttggtg
W--> 32
E--> 33 cccgaagctg 60
E--> 34 cgcggcgcgt ctgcttggtta cttgtttgac tgttggaatt gtttgtcttc
W--> 35
36 tttgtgacct 120
E--> 37 gactgtgggt ttctggacgt gttgtgtctg ttagtgtctt ttgactttt
W--> 38

*Adm
error*

PAGE: 2

RAW SEQUENCE LISTING

PATENT APPLICATION US/09/490,609

 DATE: 02/15/2000
 TIME: 14:15:54

Input Set: I490609.RAW

39 gtttcgtggt 180
 E--> 40 tgaatttgga ctgacgactg tgttta
 41 206

42 <210> 3
 E--> 43 <211> 74
 44 <212> DNA
 45 <213> Rattus norvegicus
 46 <400> 3
 E--> 47 gatccatgat actgcatgct agattttcat gtgaatattc tgattgttcg
 W--> 48
 E--> 49 atgttggttg 60
 E--> 50 cctgtttttg tttta
 51 74

52 <210> 4
 E--> 53 <211> 207
 54 <212> DNA
 55 <213> Rattus norvegicus
 56 <400> 4
 E--> 57 gatccatggt caaacaatac cgagtgatgg agacattttc actttttacga
 W--> 58
 E--> 59 gacgtgaacc 60
 E--> 60 tattgggggtg tgtggccttg tcatcccttg gaattttcca ctgcttatgt
 W--> 61
 62 tcattttgaa 120
 E--> 63 gatagccctg ccttcagctg tgggaacaca gtggctgtca agccagcaga
 W--> 64
 65 gcaaactcct 180
 E--> 66 ctcaactgctc ttcacatggc atctttta
 67 207

68 <210> 5
 E--> 69 <211> 147
 70 <212> DNA
 71 <213> Rattus norvegicus
 72 <400> 5
 E--> 73 gatccacaat gggcagaagt tagtggttcc caggattgct gggagcatgg
 W--> 74
 E--> 75 cactgtcaaa 60
 E--> 76 tcactaccgc tctgaagatt tattagacgt tgacactgct gccggaggat
 W--> 77
 78 tcagcagaga 120
 E--> 79 cagggactga actactgtct cccttta
 80 147

81 <210> 6
 E--> 82 <211> 366
 83 <212> DNA

Please Note: <213> Rattus norvegicus

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.